



Docket No.: CL000685

Serial No.: 09/748,127

Inventors: YAN, Chunhua et al.

Title: ISOLATED HUMAN DRUG-METABOLIZING...

```
1 TTTCTTCTGT TTGCTTACTC CCTATCCGGG GGCCCAAGGC GCTGTCTCCG
51 CCGCCCAAGC CCCGCGTAAA CCTGGGTGAC CTCGGAGACA TCCGTTGGAG
101 CATGAGTTCC CGACATCAGG CGGCGGCGGT GGTCCGGGAG AAACCCGGCG
151 GCGGGGAGAT AAGCCTGCCC AGGAGGCAGG GGGCTGGGCT AGCTGCCCCG
201 CCCCCGCGCT GACTTCGTTG GGGAGGGAGA CGCCCGGCTC CCGCCCTAA
251 CTAGCCAGC CGCGCGGAGC GCCTGGGAGA GGAGAAGGAG CCGACCTGCC
301 GAGATGGAGG CGACCGGCAC CTGGGCGCTG CTGCTGGCGC TGGCGTGCT
351 CCTGCTGCTG ACGCTGGCGC TGTCCGGGAC CAGGGCCCGA GGCCACCTGC
401 CCCCCGGGCC CACGCCGCTA CCACTGCTGG GAAACCTCCT GCAGCTACGG
451 CCGGGGGCGC TGTATTACAG GCTCATGCGG CTGAGTAAGA AGTACGGACC
501 GGTGTTTACC ATCTACCTGG GACCTTGGCG GCCTGTGGTG GTCTGTGGTG
551 GGCAGGAGGC TGTGCGGGAG GCCCTGGGAG GTCAGGCTGA GGAGTTCAGC
601 GGCCGGGGAA CCGTAGCGAT GCTGGAAGGG ACTTTTATG GCCATGGGGT
651 TTTCTTCTCC AACGGGGAGC GGTGGAGGCA GCTGAGGAAG TTTACCATGC
701 TTGCTCTGCG GGACCTGGGC ATGGGGAAGC GAGAAGGCGA GGAGCTGATC
751 CAGGCGGAGG CCGGTGTCTT GGTGGAGACA TTCAGGGGA CAGAAGGACG
801 CCCATTGATG CCCTCCCTGC TGTGGGCCA GGCCACCTCC AACGTAGTCT
851 GCTCCCTCCT CTTTGGCCTC CGCTTCTCCT ATGAGGATAA GGAGTTCAG
901 GCCGTGGTCC GGCAGCTGGT TGGTACCCTG CTGGGAGTCA GCTCCAGGG
951 GGGTCAGACC TACGAGATGT TCTCTGGTT CCTGCGGCC CTGCCAGGCC
1001 CCCACAAGCA GCTCCTCCAC CACGTCAGCA CCTTGGCTGC CTTTACAGTC
1051 CGGCAGGTGC AGCAGCACCA GGGGAACCTG GATGCTTCGG GCCCCGACG
1101 TGACCTTGTC GATGCTTCC TGCTGAAGAT GGCACAGGAG GAACAAAACC
1151 CAGGCACAGA ATTCACCAAC AAGAACATGC TGATGACAGT CATTTATTTG
1201 CTGTTTGTCT GGACGATGAC GGTGAGCACC ACGGTCGGCT ATACCTCCT
1251 GCTCCTGATG AAATACCTC ATGTCCAAA GTGGGTACGT GAGGAGCTGA
1301 ATCGGGAGCT GGGGCTGGC CAGGCACCAA GCCTAGGGGA CCGTACCCGC
1351 CTCCTTTACA CCGACGCGGT TCTGCATGAG GCGCAGCGGC TGTGGCGCT
1401 GGTGCCCATG GGAATACCCC GCACCCTCAT GCGGACCACC CGCTTCCGAG
1451 GGTACACCTT GCGCCAGGGC ACGGAGGTCT TCCCCCTCCT TGGCTCCATC
1501 CTGCATGACG CCAACATCTT CAAGCACCCA GAAGAGTTCA ACCCAGACC
1551 TTTCTGGATG GCAGATGGAC GGTTCAGGAA GCATGAGGCG TTCCTGCCCT
1601 TCTCCTTAGG GAAGCGTGTG TGCCTTGGAG AGGGCTGGC AAAAGCGGAG
1651 CTCTTCTCTT TCTTACCAC CATCCTACAA GCCTTCTCCC TGGAGAGCCC
1701 GTGCCCGCCG GACACCTGA GCCTCAAGCC CACCGTCAGT GGCCTTTTCA
1751 ACATTCCCCC AGCCTTCCAG CTGCAAGTCC GTCCCACTGA CTTTCACTCC
1801 ACCACGACGA CAGATGAAG GAAGGCAACT TGGAGTGGT GGGTGCCAG
1851 GACGGTGCCT CCAGCTCAA CAGTGGGAT GGACAGGGT AATGTCTCCA
1901 GAGTGATAC TGCAAGCAGC CACATTTACA CGCCTGCAGT TGTTTTCCGG
1951 AGTCTGTCCC ACGGCCACA CGCTCACTG ACTCATGCTG CTAAGATGCA
2001 CAACCGCACA CCCATACACA ACTACAAGGG CCACAAAGCA ACTGCTGGGT
2051 TAGCTTTCCA CAGACATAAA TATAGTCCAT CTGCAATCAC AAGCACATAG
2101 CCAGGTAACC CACCAACTCC CTTGGATCTG CAGCCACAC GTGGGAGTCT
2151 GGCTGTACCC TTCACAAGCC ACAGAAACGG CCACACATGT TCACAGCTCA
2201 CACGCCCTCT CCATTATCG AACTTCTCAG TGTCCCTGTC CCTGGTGCCT
2251 GGCACAGGGA ACAGCATGCC CCCTCCGGGG TCATGCCACC CAGAGACTGT
2301 CGCTGTCTAT GGGCCCAACT CATGCTCCCT CTCTTGGCTA CACCACTCTC
2351 CCAGCCTGTG ACCACCGATG TCCACACACC CCCAACCACT TGTCCACACA
2401 GCTACCCACG TACGACATCG TCCTGGCTCC CCAGAGTATC TTCCCACTGA
2451 GACACGCGCG CCCACAGAG GCACAGTCCC CAGCCACCTC TGCAACTGCA
2501 GCCCTCAGTC ACCCTTTTTT AAGCACCTG ATTCTACCA ATGCAAAAC
2551 ATCTGGGTCT GCGATTATGC ACAGAGACTT TGGACATACG AGGACCCTCA
2601 GACCGGAGGA ACACCTGCC AACCACAACA CGTGCTTATG TAACCACGTG
2651 GAAAGCGGCC CCTGCTGCC CTCCACACAC ACATACACAC TCACTGATCT
2701 ACAGCCCCCTG TTCGGCGTCA GAGTCCCCAC TAGACCCAGT GGAAGGGGTT
2751 AGAGACCAAG TAGGGGCCAG TTTCCAATTC ACCCTGTGAG GGAGTGAGCC
2801 GGATCTGACG TTCCTGTGA CTTAAGGGTC CGGCTTGGGA ATTAAGTTT
2851 GTTCTGGCC TTTAGCCTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2901 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA (SEQ ID NO:1)
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FEATURES:

5'UTR: 1-303

Start Codon: 304

Stop Codon: 1815

3'UTR: 1818

FIGURE 1A



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HOMOLOGOUS PROTEINS:

gi 117254 sp P24461 CPG1_RABIT CYTOCHROME P450 2G1 (CYP1IG1) (P...	516	e-145
gi 404777 gb AAA31432.1 (L10912) cytochrome P-450 2B-Bx [Oryct...	513	e-144
gi 479930 pir S35666 cytochrome P450 2B4 isoform Bx - rabbit >...	513	e-144
gi 117212 sp P00178 CPB4_RABIT CYTOCHROME P450 2B4 (CYP1IB4) (P...	508	e-143
gi 320075 pir S31277 cytochrome P450 2B4-B1 - rabbit >gi 21369...	508	e-143
gi 4731350 gb AAD28466.1 (AF128849) cytochrome P450 2B10 relat...	508	e-143
gi 3123191 sp P04167 CPB2_RAT CYTOCHROME P450 2B2 (CYP1IB2) (P4...	508	e-143
gi 117213 sp P12789 CPB5_RABIT CYTOCHROME P450 2B5 (CYP1IB5) (P...	507	e-142
gi 89973 pir A27717 cytochrome P450 2B5, hepatic (form HP1) - ...	507	e-142
gi 2144292 pir O4RTP2 cytochrome P450 2B2 - rat	506	e-142

EST:

gb BE148597 BE148597 MR0-HT0241-150500-010-b02 HT0241 Homo sapi...	1091	0.0
gb BF359243 BF359243 RC6-ET0072-150600-011-F01 ET0072 Homo sapi...	779	0.0
gb AW753778 AW753778 RC1-CT0286-301099-011-f08 CT0286 Homo sapi...	652	0.0

EXPRESSION INFORMATION FOR MODULATORY USE:

gb BE148597	head_neck
gb BF359243	lung_tumor
gb AW753778	colon

Tissue expression:

Human leukocyte

FIGURE 1B



```
1 MEATGTWALL LALALLLLLT LALSGTRARG HLPPGPTPLP LLGNLLQLRP
51 GALYSGLMRL SKKYGPVFTI YLGPWRPVVV LVGQEAVREA LGGQAEFSG
101 RGTVAMLEGT FDGHGVFFSN GERWRQLRKF TMLALRDLGM GKREGEELIQ
151 AEARCLVETF QGTEGRPFDP SLLLAQATSN VVCSLLFGLR FSYEDKEFQA
201 VVRAAGTLL GVSSQGGQTY EMFSWFLRPL PGPHKQLLHH VSTLAAFTVR
251 QVQHQHGNLD ASGPARDLVD AFLKMAQEE QNPGTEFTNK NMLMTVIYLL
301 FAGTMTVSTT VGYTL LLLMK YPHVQKWVRE ELNRELGAGQ APSLGDRTRL
351 PYTDAVLHEA QRLLALVPMG IPRTLMTTR FRGYTLPQGT EVFPLLGSIL
401 HDPNIFKHPE EFNPDRLDA DGRFRKHEAF LPFSLGKRVC LGEGLAKAEL
451 FLFFTTILQA FSLESPCPPD TLSLKPTVSG LFNIPPAFQL QVRPTDLHST
501 TQTR (SEQ ID NO:2)
```

FEATURES:

Functional domains and key regions:

Prosite search results:

[1] PDOC00004 PS00004 CAMP_PHOSPHO_SITE

CAMP- and cGMP-dependent protein kinase phosphorylation site

128-131 RKFT

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE

Protein kinase C phosphorylation site

Number of matches: 6

```
1 61-63 SKK
2 99-101 SGR
3 248-250 TVR
4 288-290 TNK
5 378-380 TTR
6 473-475 SLK
```

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE

Casein kinase II phosphorylation site

Number of matches: 3

```
1 119-122 SNGE
2 192-195 SYED
3 343-346 SLGD
```

[4] PDOC00008 PS00008 MYRISTYL

N-myristoylation site

Number of matches: 10

```
1 51-56 GALYSG
2 109-114 GTFDGH
3 115-120 GVFFSN
4 188-193 GLRFSY
5 207-212 GTLLGV
6 257-262 GNLDAS
7 284-289 GTEFTN
8 339-344 GQAPSL
9 370-375 GIPRTL
10 444-449 GLAKAE
```

[5] PDOC00009 PS00009 AMIDATION

Amidation site

Number of matches: 2

```
1 140-143 MGKR
2 435-438 LGKR
```

[6] PDOC00029 PS00029 LEUCINE_ZIPPER

Leucine zipper pattern

Number of matches: 2

```
1 32-53 LPPGPTPLPLLGNLLQLRPGAL
2 39-60 LPLLGNLLQLRPGALYSGLMRL
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[7] PDOC00081 PS00086 CYTOCHROME_P450
Cytochrome P450 cysteine heme-iron ligand signature

433-442 FSLGKRVCLG

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	5	25	2.305	Certain
2	64	84	0.783	Putative
3	170	190	1.041	Certain
4	292	312	2.031	Certain
5	448	468	1.133	Certain

FIGURE 2B



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BLAST Alignment to Top Hit:

>gi|117254|sp|P24461|CPG1_RABIT CYTOCHROME P450 2G1 (CYP11G1)
(P450-NMB) (OLFACTIVE)
pir||B31944 cytochrome P450 2G1 - rabbit
Length = 494

Score = 516 bits (1315), Expect = e-145
Identities = 248/491 (50%), Positives = 345/491 (69%), Gaps = 3/491 (0%)

Query: 1 MEATGTWALLLALAL-LLLLTLALSCTRARGHLPPGPTPLLLGNLLQLRPGALYSGLMR 59
ME G + + LAL LL+ +A + G LPPGPTP+P LGNLLQ+R A + ++
Sbjct: 1 MELGGAFTIFLALCFSCLLILIAWKRVQKPGRLPPGPTPIPLGNLLQVVRTDATFQSFLK 60

Query: 60 LSKKYGPVFTIYLGWPWRPVVVLVGQEAVERALGGQAEFSGRGTVAMLEGTDFGHGVFFS 119
L +KYGPVFT+Y+GP RPVV+L G EAV+EAL +A+EFSGRG +A +E F GHGV +
Sbjct: 61 LREKYGPVFTVYMG-PPVILCGHEAVKEALVDRADEFSGRGELASVERNFQGHGVALA 119

Query: 120 NGERWRQLRKFTMLALRDLGMGKREGELIQAEARCLVETFGTEGRFPDPSLLLAQATS 179
NGERWR LR+F++ LRD GMGKR EE IQ EA L+E F+ T+G P DP+ L++ S
Sbjct: 120 NGERWRILRRFSLTILRDFGMGKRSEIERIQEEAGYLLEFRKTKGAPIDPTFFLSRTVS 179

Query: 180 NVVCSLLFGLRFSYEDKEFQAVVRAAGGTLVGSSQGGQTYEMFSWFLRPLPGPHKQLLH 239
NV+ S++FG RF YEDK+F +++R + + +S+ Q Y+M+S ++ LPG H ++ +
Sbjct: 180 NVISSVVGSRFDYEDKQFLSLLRMINESFIEMSTPWAQLYDMYSGVMQYLPGRHNRYY 239

Query: 240 HVSTLAAFTVRQVQHQGNLDASGPARDLVDAFLKMAQEEQNPGTEFTNKNMLMTVIYL 299
+ L F +V+ ++ +LD P RD +D FL+KM Q++ NP TEF KN+++T + L
Sbjct: 240 LIEELKDFIAARVKVNEASLDQNP-RDFIDCFLIKMHQDKNNPHTEFNKLNVLTTLNL 298

Query: 300 LFAGMTVSTTVGYTLTLLMKYPHVQKWVREELNRELGAQAPSLGDRTRLPTDAVLHE 359
FAGT TVS+T+ Y LL+MK+P VQ + EE+N+ +G + PS+ DR ++P+TDAV+HE
Sbjct: 299 FFAGTETVSSTLRYGFLIMKHPEVQTKIYEEINQVIGPHRIPSVDREVMPFTDAVIHE 358

Query: 360 AQRLLALVPMGIPRTLMTTRFRGYTLPGQTEVFPLLSILHDPNIFKHPEEFNPDRFLD 419
QRL +VPMG+P ++R T FRGY LP+GT+VFPLLS+L DP F HP++F P FLD
Sbjct: 359 IQRLTDIVPMGVPHNVIRDTHFRGYLLPKGTDVFPPLLSVLKDPKYFCHPDDFYQHFELD 418

Query: 420 ADGRFRKHEAFLPFSLGKRVCLGEGALAEFLFFTTILQAFSLESPPCDTSLKPTVS 479
GRF+K+EAF+PFS GKR+CLGE +A+ ELFL+FT+ILQ FSL PP + + P +S
Sbjct: 419 EQGRFKKNEAFVFPSSGKRICLGEAMARMELFLYFTSILQNFSLHPLVPPVNIDITPKIS 478

Query: 480 GLFNIPPAFQL 490
G NIPP ++L
Sbjct: 479 GFGNIPPTYEL 489 (SEQ ID NO:4)

Hmmer search results (Pfam):

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
PF00067	Cytochrome P450	594.4	6.9e-175	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00067	1/1	33	493 ..	1	497 []	594.4	6.9e-175

FIGURE 2C



1	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
51	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
1951	TTGGATCGAA	GAGGTCACAG	CACCCCTCCTC	TTTCTTCCTC	CCTACCCCCA
2001	GCTGAGTAAG	AAGTACGGAC	CGGTGTTTAC	CATCTACCTG	GGACCCCTGGC
2051	GGCCTGTGGT	GGTCCTGGTT	GGGCAGGAGG	CTGTGCGGGA	GGCCCTGGGA
2101	GGTCAGGCTG	AGGAGTTTCA	CGGCCGGGGA	ACCGTAGCGA	TGCTGGAAGG
2151	GACTTTTGAT	GGCCATGGTA	AGTCAAGGGC	TGCTAGGCCC	TCCGCTCACA
2201	GCCTGCCACC	ACTTACTGGT	GTGTGACCTT	TGCACATGGC	TTAGTCCCTC
2251	TGTTGCCTCA	TCTGTCAAAT	GGAGTGATAA	CAGTGCCCAT	CAGCCGGGTG
2301	CAGTGGCTAG	TGCTGAAAT	CCCAACACTT	TGGGAGGCGG	AGGTGGGTGG
2351	ATCACTTGAG	GTCAAGAGTT	CGAGACCAGC	CTGGCCAACA	TGGTGAAACC
2401	CTGTCTCTAC	TAAAAATATA	AAAATTAGCT	GGGCACTGGT	GTGCTACCT
2451	GTAATCCAG	ATACTTGGGA	GGTTGAGGCA	GGAGAATCGC	TTGAACCCGG
2501	GAGGCAGATG	TTGCAGTGAA	CCAAGACTGT	GCCACTGCAC	TCCAGTCTGG
2551	GCAACAGATG	GAGCCTCCAT	CTCAACAACA	CAAAACAAAA	GCAGTGCCCA
2601	TCATGTAGGA	TTGAGTGATT	GAGTGAGGAC	TGAGCCTTGT	GCAAAGTGAG
2651	CACCTACTAA	TCACCAGGTT	GTAGTATCAG	TGATAACCAT	CAATGATCCA
2701	GGTAAAGCCC	TGAGGGTTCA	GAAAGATGCC	GGAGCGCTTT	CAAGGTGCTG
2751	GGGATTGGTG	GGCAAGCCCT	CGAATAATAG	AAACAGTTCT	CTGTATTACA
2801	ACAGAAAGCA	GGAGGCCCAT	GCTGGGTGCT	GCCAGGAAGT	CAGTAGTAAC
2851	TAAGACAGCA	CCGGTGCTGC	TTCCCCAGCG	CACCTAGGCC	AGTGGGGAAA
2901	CAGACTCACC	ACACAGTCCC	AGCCCCAGAGT	GGTCAGGGCC	AAGATGGGGA
2951	AGCACGGGGA	GAAAGGTCAG	GGTGGGATGG	GGAGGGGTCA	GGGCAAGAGG
3001	GGTCAGGGCC	AGGCTGAGGG	AAGCCCTGGG	ACTGTAGGAA	TTTAGAGGAG
3051	GTACCTGACC	CGGCATGTTT	GGTGAGGGAG	ATTGAGGAAG	TCTTCCTGGA
3101	AGAGAGGCTG	TCGGAGCTGA	GACTCATAAG	ATGAGTGGGG	AGGGTGTTC
3151	AGGCAGAAAG	ACGACACCT	ACAAAAGCAT	GACTTTGAGA	GAAGCATTCA
3201	TCCATTCAAC	TGATGAATTT	TCAGACTGGG	CACGCTGGCT	CATGCCTGTA
3251	ATCCCAGCAC	TTTGAAGGC	TGAATGGGGA	GGATGACTTG	AGCCTAGGCA
3301	TTTGTGACAA	GCTTGGGCAA	CATGGTGAGA	CCCTGCCTCC	ACAAAAACAA
3351	CAAACAAACA	AAAAATCATT	ATACCTGGTA	CCATGGGTAC	CAGGTACATA
3401	GAAATGACTC	AGGCAGATAT	GGTGTCTCT	CCTACTGTGG	GAGAGGCGGG
3451	CTTATACTGC	AGTAAGACAA	TAGAGGGAGG	GAATATAATC	CTAAAATGAG
3501	AGGTACAGAT	TTGAGAGCAA	ACACAGGGCA	CAGGCATATG	TACGAGGGTA
3551	AAGAGGGAAT	CAGGGAAGGC	TTCTCAGAGA	AGGTGACATT	TAAGCCGGGA
3601	CATGAAGGAT	GACAGAGTTA	GTTACCAAG	GATGGGATGG	AAAGGGGTGA
3651	GAGTGATGGA	GGCAGAGGGA	ACTGCAGGAT	CATAGGCCTA	GACAGGGGAT
3701	CCTGACGCCC	TTGAGGAAGT	GAGAGAAGAC	CAGCGCAGTC	GTAGTGGGTT
3751	AAGTAACAAA	GCTGAGAAGC	CAGGGAATC	CCTGGTCATG	CAGGGCCTGT
3801	GAGTCACGTC	AGAGTGTTTG	GGCTTTTGT	TTTCCTGGGA	GCACTCGATT
3851	TTAAGCAGGG	AACAGCTGTA	TTCAGAGTTG	GGAAGATCCT	GTGGTTGCTG

FIGURE 3A



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3901 CCTGAAGGGG ATGAAACTGG AGGCTAGGAG CCCAGGGTGA TAGGGAGGAT
3951 CCAGGGTGAT GGGGAGGCTG GGAGGTCCCG GGTGATGGAC CAGGGCTGGG
4001 GCCAGGGGAT GGGGAGGAAG GAGTAATTGG GAGAGGCTG GGGCTCTGGC
4051 CGAGGAATGG ATGGTGGGCT GAAACAGGGA GAGGAGAGAT GCTTAGGCCA
4101 CTTTGGAACA CAGTAGGGCA AGGACAGGAG ACACCCAAGG GGAAGTGCCC
4151 AAGAGACCAC GACAGGCTGG CATTGGACAG GGAAGGTCTG TCTGGAGCAG
4201 GTGTCTTGGG TAAGGGAGGA AAATGGTGCA GTTCCATCCT CCTCCCTCTC
4251 TGTTCAACCT CTAACACTACA TGGGGCACAG GACCCAGTGG GACTCCATAA
4301 ATGATGGGAT GGGTGGATGG AAGGAAGGAA GGAGGAAACA ACTCTTCATT
4351 CATCCTGGTT ATTTACAGAA CAGGCCAGGT GCGGTGCTCA CGCTTGCCAT
4401 TCTAGCACTT TGGGAGGCTG AGGTGGGTGG ATTACCTCAG GTCAGGAGTT
4451 CAAGACCAGC CTAGACAACG TAGAGAAACC CCATCTCTAC TGAAGATATA
4501 AAATTAGCTG GGCCTAGTGG CATATGCCTG TAATCCCAGC TAGTCGGGAA
4551 GCTGAGGCAG GAGAATCGCT TGAACCCGAG AGGCAGAGGT TGCCTGAGC
4601 TGAGATCGTG CCATTGCACT CCAGCCTGGG TGACAAAGCA AGACCTCGTC
4651 TCAATAATAA TAATAATTAC AAAACAGAAG GAGCCTGGGT CATCCAGCT
4701 ACCTACTTTT CAGGAGAATG TACTCCCTTA CCCAAGGGCA AAGGATGGGA
4751 GAACCACTTT GATTATGCAT TTATTGAGCA CTTACTGAGT CCTCATCCCT
4801 GGGCTAGGCT GGAATGGACT CAGATGGAGC CTGAAGAGTC CCCCTCAGGG
4851 AACCTCACTA GAAAGAAGGA GGAATCGGCC GGGCGCGGTG GCTCACGCCT
4901 GTAATCCCAA CACTTTGGGA GGCTGAGGTG GGTGGATCAC AAGGTCAGGA
4951 GATCGAGACC ATCCTGGCTA ACACAGTGAA ACCCATCTC TACTAAAAAT
5001 ACAAAAAATG AGCCAGGCAT GGTGGCGGGC GCCTGTAGTC CCAGCTACTC
5051 AGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CCGGGAGGCA GAGGTTGCAG
5101 TGAGACGAGA TCACGCCACT GCACTCCAGC CTGGGCAACA GAGCGAGATT
5151 CCGTCTCAAA AAAAAAAGA AAGAAAGGAA GAAGGGGGAA TGGGGGAGAG
5201 GGGCCGGTCC CTTTTTGGT CTAGCCTTCT GCGCAGGGGT TTTCTTCTCC
5251 AACGGGGAGC GGTGGAGGCA GCTGAGGAAG TTTACCATGC TTGCTCTGCG
5301 GGACCTGGGC ATGGGGAAGC GAGAAGGCGA GGAGCTGATC CAGGCGGAGG
5351 CCGGTGTCTT GGTGGAGACA TTCAGGGGGA CAGAAGGTCA GCATGGCGGG
5401 GTCACCCAGG GGTCTCCAGC CGAGTGAAAG GGAAGAACTC CTTACTGTGG
5451 CTGGGGGTGG CCCCACCCCA GGTCTGGAA TGGGCAGGAG GGAAGCCTT
5501 GAACTTAGG GCTGGCCTGG GGGTTCTGTT CACTGCCACC TTCTGTCTCT
5551 GTCCCACTGT CTCTCCGAGG CTGTCATGAC ATCTCTCTGT GTGTCTCTGG
5601 TGCTATCATC CCATCTCTCC TGGGTCTCCA TCTCTCTCTC TGCTCTTTTT
5651 CTTTCTCTCT CTTTCTCTCT ATTTTTTGGG CCCTCAGTCT ATCTCTGTTT
5701 CTGTCTCCCT GTCTGTGTGA TGGTCACTCT GTTCTTTTCT CCCTGTCTGT
5751 TTCTCTGTCC CTATCTGTCT GTATCCTTCT TTGCCTGTTT AGCTCTCTCC
5801 CTGCGCTGTC CATCCATCTT TCCTGCCTC CCTGTCTCTC TCTGGTTGGG
5851 TTCAGCCCCA ACCTGCTCCC CTCTGCCTGG CTCCATCACA GCCTACCTCC
5901 CTGCCCCCAT TCCCCCAGG ACGCCCATTC GATCCCTCCC TGCTGCTGGC
5951 CCAGGCCACC TCCAACGTAG TCTGCTCCCT CCTCTTTGGC CTCCGCTTCT
6001 CCTATGAGGA TAAGGAGTTC CAGGCCGTGG TCCGGGCAGC TGGTGGTACC
6051 CTGCTGGGAG TCAGCTCCCA GGGGGGTGAG GTGAGTGGGT GGGACCCCTC
6101 TCCAACCTAC TTCCCTGAAG GTTCTGCCA AGGTCCCAGT AGAAGTAGCT
6151 GCCCTTCTCC CCACAGACCT ACGAGATGTT CTCCTGGTTC CTGCGGCCCC
6201 TGCCAGGCCC CCACAAGCAG CTCTCCACC ACGTGAGCAC CTTGGCTGCC
6251 TTCACAGTCC GGCAGGTGCA GCAGCACCAG GGGAACTGAG ATGCTTCGGG
6301 CCCCGCAGCT GACCTTGTG ATGCTTCTCT GCTGAAGATG GCACAGGTGT
6351 GGGAGGGGTG CAGGGACCCC CTCTCTGAAT GGGCGTGGTG ACCTGGCAGG
6401 TCCCAGCCAG GTGTCCCTGG GGACCTCAAT TGGGTTCCTC TCTCTTTCTC
6451 TCTCTGCATG TCTCTGTGAG TATGAGTGTC TCTGTGCATG TGTGTGCATC
6501 CCTCTCTGCT ACATCTGTGC TGGCCCTTTC AGGGCGTTGC TCTCACTGCC
6551 TCTCCCGCCC CCGACCTGGG CATTTGTGCC GGGCTGTCTG TCTCTCCAGC
6601 ATCTCTCCTC TTCTCCCTC CCACCTCGGC CCTTGTGTTT AGGCCCCATG
6651 CCCAGGGTCC TACACCAGCA ATCCCCAGGA TCACTTCATC CCATCCCCTG
6701 CAGCTCTCCC AGACTTTTAT GTAATTACAC AATTTTATGT GAATTATGGT
6751 CATTTATTAG GAAGCCTTGC AATATCAAGT TATGTTAATA AAGTCCAATT
6801 TATTAATTAT ATAAGAACA TATTTCTTTT CCTTTTTTTT TTCTTTTCTT
6851 TTTAAAGAGA CAGGATCTCT TTCTGTTGCC CAGGCTAGAG TACAGTTGCA
6901 AAATCATAGC TCACTGCAAC CTTGAACTCC TGGGCTCAAG CAATCCTCCT
6951 GCCTCGGGCT CTTGAGTAGC TGGGACAACA GGTGTGCACC ACCACACCTG
7001 GCTAAATTTT TTTTTTTCT TTGTAGAGAT AGACTCTCAC TATGTTACCC
7051 AGGCTGGTCT TGAATTCCTG GGCTCATGTA ATCCTCCTGC TGCTTTGAAC
7101 TCCCAAAGTG CTGGGACTAT AGGCATAAGA CATCATGCCC GGTCGGGCAC
7151 AGTGGCTCAT GCCTGTAATC TCAGGACTTT GGGAGGCCGA GACGGGCGGA
7201 TCACCTGAGG TCGGGAGTTC GAGACCAGCC TGACCAACAT GGAGAAACCC
7251 CATCTCTACT AAAAAAATA ATACAAAATT AGCCGGACGT GGTGGCACAT
7301 GCCTGTAATC CCAGCTACTA GGGAGGCTGA GGCAGGAGAA TCGCTTGAAC
7351 CCGGGAGGCT TAGGTTGCGG TGAGCTGAGA TTGCACCAT GCACCTCAGC
7401 CTGGGCAACA AGAGCGAAAT TCCATCTCAA AAAAAAATAA AAAGAAAAAA
7451 AGAAAAAAGA CACCATGCCC TATAAGTAAA CTAGAATTAA GGTGACTCCT
7501 AAGGAAATAA ATAGTTTTTA ACTGTACGAA CTTTGGGAAG AATGGGGCCA
7551 ATTCTTTAAT TAAATGCAGC CTCCTGTGTT GTGGAGAAAG AAAAATTTTT
7601 CTTAACCTTA TTGCCCCATT TCTTTTCTCT TTTATTGAAT ATTTTTTAGT
7651 TTTAACTATA TTAAAAATACA CATAACGTTT ACCATCTTAA CCATTTTTAG
7701 GTATACAGTA CAGTAGTGT CAGTACATTC ATACTGTTAT GCAATCAGTC
7751 TCCAGAACTC TTCATGTTGC AAAGCTGAAA CTCTATACCC ATTAACAAAC

FIGURE 3B



7801	TGCCTGTTCC	TCCCTCCTCC	AACCCCTGGC	AATCACCTTT	TTTTTTTTGA
7851	GACGAAGTCT	CACTCTGTCA	CCCAGGCTAG	AGTGCGGTGG	CTCGATCTCG
7901	GCTCACTGCA	AGCTCCGCCT	CCCGGGTTCA	TGCCATTCTC	CTGCCTCAGT
7951	CTCCAAGCA	GCTGGGACTA	CAGGTGCCCG	TCACCACGCC	TGGCTAATTT
8001	TTTGATATTT	TAGTAGAGAT	GGAGTTTCAT	CGTGTTAGCC	AGGCTGATCT
8051	CAAACTCCTG	GCCTCAAGTG	ATCCACCCGC	CTCGGCCTCC	CAAAGTGCTG
8101	GGACTACAGG	CGTGAGCCAC	TGTGCCTGGC	CAGGAAGTAG	ACTCTTGATA
8151	TTAGTTCTCT	CTGGTTGAAA	TGTTTTTAAA	AATGAAAGAG	AATGACTAAT
8201	AACAAAAACA	CAGAAAGTTA	TAAGGATTGA	TGAAGATGTG	GAGACTTTGA
8251	AACCCATGTA	TACCATTGGT	GGGAATGTGA	AACGACGCAG	CCCTGTGGAA
8301	AATGGTACAG	CAGTTACCTG	AGGTGAGGAG	TTTGAAACCA	ACCTGGCCAA
8351	CATGCAGAAA	CCCCGTCTCC	ATTAATGTGA	CAAAAATTAG	CCAGGNNNNN
8401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
8951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
9951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
10951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN

FIGURE 3C

OIP E 301A
DEC 20 2002
PATENT & TRADEMARK

Docket No.: CL000685
Serial No.: 09/748,127
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN DRUG-METABOLIZING...

11701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
11951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
12651	CCCTTCTCTC	CTTCTCTCTC	TCCTGTCTTC	CTCTCTTTCT	CTCTTTCTTT
12701	CTTGACAGGG	TCTCTCTTTG	TCTCCAGGC	TGGGGTGCAG	TGGTACAAGC
12751	ATAGCTCACA	GCAGCCTTGA	ACTCCTAGGC	TCAAGTGATC	CTCCACGTC
12801	AGCCTCTGA	GCAGCTGGGA	CAACGGGCTC	ATACCACCAT	GCCTGGCTAA
12851	TTTTTTAATT	TTTCGTAGAG	ACAAGGTCTT	GTTATATTGC	CCAGGCTGGT
12901	CTCAAATCC	TGGGCTCAAA	TGCTTCTCTC	ACCTCAGCCT	CCCACGTGGC
12951	TGGGATTACA	GGCATGAGCC	ACTGCACGCC	ACTCAACACT	CCACAAATGT
13001	TGATGCCATT	ATGTTTTGTG	AACTAGTGTC	CCTGGCACCC	GAGACTTGTA
13051	CTCCACACTC	GAGGACCAAA	TAGACTGGGG	TGGGAAGGGG	TTTATAGTTT
13101	CATTATTATT	TCCCTCAGG	GCACGGAGGT	CTTCCCCCTC	CTTGGCTCCA
13151	TCCTGCATGA	CCCCAACATC	TTCAAGCACC	CAGAAGAGTT	CAACCCAGAC
13201	CGTTTTCTGG	ATGCAGATGG	ACGGTTCAGG	AAGCATGAGG	CGTTCCTGCC
13251	CTTCTCTTAA	GGTATCTGCT	GCAGCCCTGG	GTATCACAAG	CAGGTGCTGG
13301	CGAACTCCAG	GCATCTGTGC	CAGCTGGGGG	CACCCCTCTG	CACCCCTGGG
13351	TTACTGTTGG	CTCCTCCACC	TGCTGTTCCC	CCCGTGGGCC	TGGGTGTGAG
13401	GAATACTGAC	TCAGCCCTCT	CTCTCTCTCT	CTCTCACCA	GGAAGCGTG
13451	TCTGCCCTGG	AGAGGGCCTG	GCAAAAGCGG	AGCTCTTCCT	CTTCTTCACC
13501	ACCATCTTAC	AAGCCTTCTC	CCTGGAGAGC	CCGTGCCCGC	CGGTACACCC
13551	TGAGCCTCAA	GCCCACCGTC	AGTGGCCTTT	TCAACATTCC	CCCAGCCTTC
13601	CAGCTGCAAG	TCCGTCCCAC	TGACCTTCAC	TCCACCACGC	AGACCAGATG
13651	AAGGAAGGCA	ACTTGGAAGT	GTTGGGTGCC	CAGGACGGTG	CCTCCAGCCT
13701	CAACAGTGGG	CATGGACAGG	GTTAATGTCT	CCAGAGTGTA	CACTGCAGGC
13751	AGCCACATTT	ACACGCCTGC	AGTTGTTTTT	CGGAGTCTGT	CCCACGGCCC
13801	ACACGCTCAC	TTGACTCATG	CTGCTAAGAT	GCACAACCGC	ACACCCATAC
13851	ACAACACAAA	GGGCCACAAA	GCAACTGCTG	GGTTAGCTTT	CCACAGACAT
13901	AAATATAGTC	CATCTGCAAT	CACAAGCACA	TAGCCAGGTA	ACCCACCAAC
13951	TCCCTTGGAT	TGCAGGCCCA	CACGTGGGAG	TCTGGCTGTC	ACCTTCACAA
14001	GCCACAGAAA	CGGCCACACA	TGTTACAGC	TCACACGCCC	TCTCCATTCA
14051	TCGAACCTCT	CAGTGTCCCT	GTCCCTGGTG	CCTGGCACAG	GGAACAGCAT
14101	GCCCCCTCCG	GGGTCTATGC	ACCCAGAGAC	TGTCGCTGTC	TATGGCCCCA
14151	ACTCATGCTC	CCTCTCTTGG	CTACACCACT	CTCCAGCCT	GTGACCACCG
14201	ATGTCCACAC	ACCCCAACCC	ACTTGTCCAC	ACAGCTACCC	ACGTACGACA
14251	TCGTCTCTGG	TCCCCAGAGT	ATCTTCCAC	TGAGACACGC	CGCCCCCACA
14301	GAGGCACAGT	CCCCAGCCAC	CTCTGCAACT	GCAGCCCTCA	GTCACCCCTT
14351	TTTAAGCACC	CTGATTCTAC	CAAAATGCAAA	CACATCTGGG	TCTGCGATTA
14401	TGCACAGAGA	CTTTGGACAT	ACGAGGACCC	TCAGACCGGA	GGAACACCTG
14451	CCCAACCCCA	ACACGTGCTT	ATGTAACCA	GTGGAAGCG	GCCCCTGCTG
14501	CCCTCCACA	CACACATACA	CACTCACTGA	TCTACAGCCC	CTGTTCCGGC
14551	TCAGAGTCCC	CCTAGACCCC	AGTGAAGGG	GTTAGAGACC	AAGTAGGGGC
14601	CAGTTTCCAA	TTACCCCTGT	CAGGGAGTGA	GCCGGATCTG	ACGTTCTCTG
14651	TGACTTAAGG	GTCCGGCTTG	GGAATTAAG	TTTGTCTCTG	GCCTTTAGCC
14701	TACTGCGTGT	GTGACCCGTG	TCAGTCACTG	TGAGTAAGGG	GTGGGGACAG
14751	GGGAGTCCAC	CCCTCCCTTG	AGGCTGGGCG	GGAGCTGAAA	AACATGGCCA
14801	CCGCCACCC	TGGCTGTTGA	CATCAGGACC	AGATGTGGAG	CTGGGAGGAG
14851	GGGCAGGGCT	GGTGACGCC	TGGGCTCAT	TTCCAAAAG	GGCCAAGGTG
14901	TCCGGCGGTG	GGAAGTGGG	AAGGAGGGG	TAACCCAAGC	TGGACTGTGG
14951	ACCTTGGGG	CTTCTCAGC	CAGGGAGAGC	CTGAAGCCAA	CTAGATCCAG
15001	ACCCTAGAGA	CTCTTCAAAC	TTGAGTACAG	GAACTAGCTT	GCAACACAGA
15051	CTCTAAGCCC	ACTCCCATTT	CTTCCACCCT	TTTTCTCTTG	CCTCCCTTTC
15101	ACAAGGAAAC	CAGAGGCATT	TGTAATTTT	CTTTCTTTTT	TTTTTTTTTT
15151	TTTTTTTTGA	GACGGAGTCT	CACTCTGTCA	CCCAGGCTGG	AGTGCAGTGG
15201	TGTGATCTTG	GCTCACTGCA	GCCTCCGCCT	CCGGGTTCAA	GCCATTCTCC
15251	TGCCTCAGCC	TCCCAAGTAG	CTGGGATTAC	AGGTGTGTGC	CACCACGCCC
15301	AGCTAATTTT	TGATTTTTTA	GTAAGATAGG	GGTTTCACCA	TGTTGGCCAG
15351	GCTGGTCTCG	AACTCCTGAC	CTCAGATGAT	CTGCCAGTCT	CGGCCTCCCA
15401	AAATGCTGGG	ATTACAGGCG	TGAGTCGCTA	CTAGATAAAT	TTCTTATCTA
15451	GCAAAGAAGT	TGCAAAACAT	ACGCAAAAGT	AGAAAGATAC	AATGAGCCCC
15501	CAGGTGCCCA	TCACCCAGCC	TCATTTCAAT	AGTCATCAAC	TTTCTGCAGC
15551	TTTTACTTCA	TCTATATCCT	TTTCTGCCTC	TTTTTTTTTT	TTTTTATTTT

FIGURE 3D

DEC 20 2002
PATENT & TRADEMARK

Docket No.: CL000685
Serial No.: 09/748,127
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN DRUG-METABOLIZING...

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15601 GAGATAGGGT TTTGCTTTGT TGCCCAAGCT GGGGTGCAGT AGCATGATCT
15651 CATAGTTTAC TGGGGCTTCA GACTCCTAGG CTCAAGTGAT CCTCCCGCCT
15701 CGGCCTCCAA GCAGCTGGGA CTACAGATGC GTGCCACCAC ACCCAGCTAA
15751 ATTTCTTATT TTTATTTTCT ATAGAGAAAG TCTCACTATA CAGCCCTGTG
15801 CTGGTCTCAA ATTCCAGGCC TCAAGAGTTT CCATCCCAGC CTCCCAAAGT
15851 GCTGGGATTA TAGGCGTGAG TCACTGCACC CTGCCCTAAT ATTTTATTTT
15901 TATCTATTGC TTTTATTTA CTTATTTATC TTTTATTTT GAGACAGAGT
15951 CTCACTCTGT GGCCCATGCT GGAGTGCACT GGCATCATCT CGGCTCACTG
16001 TAACCTCCGC CTCTTAGGTT CAAGCAGTTC TCCTGCCTTG ACCTCCCGAG
16051 TAGCTGGAAT TACAGGTGCC TGCCACCAAG CCTGGCTAAT TTTTATTTT
16101 GTAGTAGAGA TGGGGTTTTG CCATGTTGAC CAGGCTGGTC TCGAACTCCT
16151 GACCTCAGGT GATCTGCCCA CCTTGGCCTC CCAAAGTGCT GAGATTACTG
16201 GTATGAGCCA CCGTGCCTGG CCACCTATTG CTTTTTAAAG ATTTATTTT
16251 TATTATTATT ATTTTATTTT TTGCAGATGG AGTTTCGCTA TTGTTGCCCA
16301 GGCTGGAGTG CAATGGCGTG ATCTCAGCTC ACCGCAACCT CCGCTCCCA
16351 GGTTCAGCG ATTCTCCTGC CTCAGCATCC CTAGTAGCTG GGATTACAGG
16401 CATGCACCAC CATGTCCAGC TAATTTTGTA TTTTATAGTAG AGACGAGGTT
16451 TCTCCAGGTT GGTCAAGCTG GTCTCAAACCT CCAACCTCA GGTGATCCGC
16501 CCATCTCGGC CTCCCAAAGT GCTGGGATTA CAGGTGTGAG CCACCGCGCC
16551 TGGCCTTAAA GATTATTTTA AGGCAAATTA CAGAAAGCAA TTTAATGCAC
16601 ATTTCTGAGA GTTAAAGATA TTTTGGCCT TGACATTTTA TGAGGACAGT
16651 TTTCAACAT GCAGCAAAGT TGAGGGAATT GTACAAGGAA CACCTTGTGC
16701 ACTCCTGCCT CAGTCTCCCA AGCAGCTGGG ACTCAGGTG CCGCTCACCA
16751 CGCCTGGCTA ATTTTGTGTA TTTTATAGTAG AGATGGAGTT TCATCGTGTT
16801 AGCCAGGCTG ATCTCAAACCT CCTGGCCTCA AGTGATCCAC CCGCTCGGC
16851 CTCCCAAGTG CTGGGACTAC AGGCGTGAGC CACTGTGCCT GGCCAGGTAA
16901 GTAGACTCTT GATATTAGTT CTCTCTGGTT GAAATGTTTT TAAAAATGAA
16951 AGAGAATGAC TAATAACAAA AACACAGAAA GTTATAAGGA TTGATGAAGA
17001 TGTGGAGACT TTGAAACCCA TGTATACCAT TGGTGGGAAT GTGAAACGAC
17051 GCAGCCCTGT GGAATGGT ACAGCAGTTA CCTGAGGTCA GGAGTTTGAA
17101 ACCAACCTGG CCAACATGCA GAAACCCCGT CTCCATTAAA TGTACAAAAA
17151 TTAGCCAGGC ATGGTGGTGC GCACCTGTAA TCCAGCTAC TCGGGAGGCT
17201 GAGGCAGGAG AATTGCTTGA ACCCAGGAGG CGGAGGTGCG AGTGAGCCGA
17251 GATCGTGCCA CTGCACTCAG CCTGGGCAAC AAAGCAAGAC TCTGTCTCAA
17301 AAAAAAAG TCTACTTCCC AACCTTCCCA AAAATTTATC TAAACCCCGT
17351 GACAAAACCT TAACCTGTGT TTCCGACCCC AGGCTTGGCT GTTCTGGACA
17401 TTTACTTCCC AAAGGCTGTG TTCTCTCAGC CCCTCTGCCT GGTTCCTTTC
17451 AGGAGGAACA AAACCCAGGC ACAGAATTCA CCAACAAGAA CATGCTGATG
17501 ACAGTCATTT ATTTGCTGTT TGCTGGGACG ATGACGGTCA GCACCACGGT
17551 CGGCTATACC CTCCTGCTCC TGATGAAATA CCCTCATGTC CAAAGTAAGA
17601 GCCTTTTCCA CTTGCCAGGC CTTGGGAACA GAAGTCAGGG TTCTAGGCTG
17651 AGCAAGGTGG CTCACGCCTA TAATCCCAGC ACTTTGGGAG GCTGAGGCGG
17701 GCTGATCACT TGAGAATAGG AGTTTAAAGAC CAGCCGCCCA ACACAGTGAA
17751 AC (SEQ ID NO:3)

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FEATURES:

Start:	1999	6349
Exon:	1999	2167
Intron:	2168	5236
Exon:	5237	5386
Intron:	5387	5919
Exon:	5920	6080
Intron:	6081	6166
Exon:	6167	6349
Intron:	6354	13542
Exon:	6354	6636
Intron:	6637	13087
Exon:	13088	13261
Intron:	13262	13441
Exon:	13442	13542
Intron:	13547	13648
Exon:	13547	13648
Stop:	13649	

SNPs:

DNA

Position	Major	Minor
2226	G	C A
2226	C	A G T
3081	A	T G C
3788	A	T
3979	T	C G
5056	T	C G
5213	T	G A C
5508	A	C T G
5857	C	G A T

FIGURE 3E



Docket No.: CL000685
Serial No.: 09/748,127
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN DRUG-METABOLIZING...

6385	C	T G
6813	C	T A
7853	C	T
12973	G	C T
12973	A	G T
13012	G	A C T
13072	A	T C G
13370	C	G
13682	C	T A
14631	C	T G

Context:

DNA
Position

2226 TGACAGGGGCCATGATGGAGACACCTTGGATCGAAGAGGTCACAGCACCTCCTCTTTCT
TCCTCCCTACCCCCAGCTGAGTAAGAAGTACGGACCGGTGTTCAACATCTACCTGGGACC
CTGGCGGCCTGTGGTGGTCCTGGTTGGGCAGGAGGCTGTGCGGGAGGCCCTGGGAGGTCA
GGCTGAGGAGTTCAGCGGCCGGGAACCGTAGCGATGCTGGAAGGGACTTTTGATGGCCA
TGGAAGTCAAGGGCTGCTAGGCCCTCCGCTCACAGCCTGCCACCACTTACTGGTGTGTG
[G,C,A]
CCTTTGCACATGGCTTAGTCCCTCTGTTGCCTCATCTGTCAAATGGAGTGATAACAGTGC
CCATCAGCCGGGTGCAGTGGCTAGTGCCTGAAATCCAACACTTTGGGAGGCGGAGGTGG
GTGGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAACCCCTGTCT
CTACTAAAAATATAAAATTAGCTGGGCATGGTGGTGCGTACCTGTAATCCAGATACTT
GGGAGGTTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGATGTTGCAGTGAACCAAGA

2226 TGACAGGGGCCATGATGGAGACACCTTGGATCGAAGAGGTCACAGCACCTCCTCTTTCT
TCCTCCCTACCCCCAGCTGAGTAAGAAGTACGGACCGGTGTTCAACATCTACCTGGGACC
CTGGCGGCCTGTGGTGGTCCTGGTTGGGCAGGAGGCTGTGCGGGAGGCCCTGGGAGGTCA
GGCTGAGGAGTTCAGCGGCCGGGAACCGTAGCGATGCTGGAAGGGACTTTTGATGGCCA
TGGAAGTCAAGGGCTGCTAGGCCCTCCGCTCACAGCCTGCCACCACTTACTGGTGTGTG
[C,A,Gst]

FIGURE 3F

DEC 2 0 2002
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Docket No.: CL000685
Serial No.: 09/748,127
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN DRUG-METABOLIZING...

3081 CCTTTGCACATGGCTTAGTCCCTCTGTTGCCTCATCTGTCAAATGGAGTGATAACAGTGC
CCATCAGCCGGGTGCACTGGCTAGTGCCTGAAATCCCAACACTTTGGGAGGCGGAGTGG
GTGGATCACTTGAAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTGTCT
CTACTAAAAATATAAAATTTAGCTGGGCATGGTGGTGCCTGTAATCCAGATACTT
GGGAGGTTGAGGCAGGAGAATCGCTTGAAACCCGGGAGGCAGATGTTGCAGTGAACCAAGA

3788 AAACAGTTCTCTGTATTACAACAGAAAGCAGGAGGCCATGCTGGGTGCTGCCAGGAAC
CAGTAGTAACTAAGACAGCACCGGTGCTTCCCAAGCGCACCTAGGCCAGTGGGGAAA
CAGACTCACCACACAGTCCCAGCCAGAGTGGTCAGGGCCAAGATGGGGAAGCACGGGGA
GAAAGGTGAGGTGGGATGGGAGGGGTGAGGCAAGAGGGGTGAGGCCAGGCTGAGGG
AAGCCCTGGGACTGTAGGAATTTAGAGGAGGTACCTGACCCGGCATGTTTGGTGAGGGAG
[A, T, G, C]
TTGAGGAAGTCTTCTGGAAGAGAGGCTGTGCGAGCTGAGACTCATAAGATGAGTGGGA
GGGTGTTCCAGGCAGAAAGACCAGCACCTACAAAGCATGACTTTGAGAGAAGCATTTCAT
CCATTCAACTGATGAATTTTCAAGTGGGCACGCTGGCTCATGCCTGTAATCCAGCACT
TTGGAAGGCTGAATGGGAGGATGACTTGAGCCTAGGCATTTGTGACAAGCCTGGGCAAC
ATGGTGAGACCCTGCCTCCACAAAACAAACAAACAAAAATCATTATACCTGGTAC

3979 ATCTAAATGAGAGGTACAGATTTGAGAGCAAAACAGGGCACAGGCATATGTACGAGG
GTAAAGAGGGAATCAGGGAAGGCTTCTCAGAGAAGGTGACATTTAAGCCGGGACATGAAG
GATGAACGAGTTAGTTACCAAGGATGGGATGGAAGGGGTGAGAGTGATGGAGGCAGAG
GGAATGCAAGGATCATAGGCTAGACAGGGGATCCTGACGCCCTTGAGGAAGTGAGAGAA
GACCAGGCAGTCGTAGTGGGTTAAGTAACAAAGCTGAGAAGCCAGGGAATCCCTGGTC
[A, T]
TGCAGGCCCTGTGAGTCACGTGAGTGTGTTGGGCTTTTGTCTTCTGGGAGCAGTCGA
TTTTAAGCAGGGAACAGCTGTATTGAGAGTTGGAAGATCCTGTGGTTGCTGCCTGAAGG
GGATGAACTGAGGCTAGGAGCCAGGGTGATAGGGAGGATCCAGGGTGATGGGAGGC
TGGGAGGCTCCGCGGTGATGGACAGGGCTGGGGCCAGGGGATGGGAGGAAGGAGTAATT
GGGAGAGCCTGGGCTCTGGCCGAGGAATGGATGGTGGGCTGAAACAGGGAGGAGGAG

5056 ATCATAGGCCTAGACAGGGGATCCTGACGCCCTTGAGGAAGTGAGAGAAGACCAGCGCAG
TCGTAGTGGGTTAAGTAACAAAGCTGAGAAGCCAGGGAATCCCTGGTCATGCAGGGCCT
GTGAGTCACGTGAGTGTGTTGGGCTTTTGTCTTCTGGGAGCAGTCGATTTTAAAGCAG
GGAACAGCTGTATTGAGAGTTGGGAAGATCCTGTGGTTGCTGCCTGAAGGGGATGAAACT
GGAGGCTAGGAGCCAGGGTGATAGGGAGGATCCAGGGTGATGGGAGGCTGGGAGGTCC
[T, C, G]
CGGTGATGGACAGGGCTGGGGCCAGGGGATGGGGAGGAAGGAGTAATTGGGAGAGGCCT
GGGGCTCTGGCCGAGGAATGGATGGTGGGCTGAAACAGGGAGAGGAGAGATGCTTAGGCC
ACTTTGGAACACAGTAGGGCAAGGACAGGAGACACCAAGGGGAAGTGCCCAAGAGACCA
CGAAGGCTGGCATTTGGACAGGGAAGGTCTGTCTGAGCAGGTGTCTTGATAAGGGAGG
AAAATGGTGAGTTCATCTCTCTCTCTCTGTTCACCTCTAACTACATGGGGCACA

5213 AGTTTGATTATGCATTTATTGAGCACCTACTGAGTCCTCATCCCTGGGCTAGGCTGGAAT
GGACTCAGATGGAGCCTGAAGAGTCCCTCAGGGAACCTCACTAGAAAGAAGGAGGAAT
CGGCCGGGCGGGTGGCTCAGGCCTGTAATCCCAACACTTTGGGAGGCTGAGGTGGGTGG
ATCACAAGGTGAGAGATCGAGACCATCCTGGCTAACACAGTGAACCCCATCTCTACTA
AAAATACAAAAAATGAGCCAGGCATGGTGGCGGGCGCTGTAGTCCAGCTACTCAGGAG
[T, C, G]
CTGAGGCAGGAGAATTGCTTGAACCCGGGAGGCAGAGGTTGAGTGAGACGAGATCACGC
CACTGCACTCAGCCTGGGCAACAGAGCGAGATTCGTCTCAAAAAAAAAAGAAAGAAA
GGAAGAAGGGGAATGGGGGAGAGGGGCCGTCTTTTGTAGTCTAGCCTTCTGCGCAG
GGGTTTTCTTCTCAACGGGGAGCGGTGGAGGCAGCTGAGGAAGTTTACCATGCTTGTCT
TGCGGACCTGGGCATGGGAAGCGAGAAGCGAGGAGCTGATCCAGGCGGAGGCCGGT

5508 CTTTGGGAGGCTGAGGTGGGTGGATCACAAGGTGAGGATCGAGACCATCCTGGCTAAC
ACAGTGAAACCCCATCTCTACTAAAAATACAAAAATGAGCCAGGCATGGTGGCGGGCGC
CTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGAACCCGGGAGGCAGA
GGTTGCACTGAGACGAGATCACGCCACTGCACTCCAGCCTGGGCAACAGAGCGAGATTCC
GTCTCAAAAAAAGAAAGAAAGGAAGGGAATGGGGAGAGGGGCCGTCTCT
[T, G, A, C]
TTTGAGTCTAGCCTTCTGCGCAGGGGTTTTCTTCTCAACGGGGAGCGGTGGAGGCAGCT
GAGGAAGTTTACCATGCTTGTCTGCGGGACCTGGGCATGGGGAAGCGAGAAGGCGAGGA
GCTGATCCAGGCGGAGGCCCGGTGTCTGGTGGAGACATTCAGGGGACAGAAGGTGAGCA
TGGCGGGGTCAACCCAGGGTCTCCAGCCGAGTGAAAGGGAAAACTCTCTACTGTGGCTG
GGGTGGCCCAACCCAGGTCTGGAATGGGCAGGAGGGAAGCCTTGAACCTAGGGCT

FIGURE 3G

Serial No.: 09/748,127

Title: ISOLATED HUMAN DRUG-METABOLIZING...

CTGTCTCTCCGAGGC TGT CATGACATCTCTCTGTGTGTCTCTGGTGCTATCATCCCATTCT
TCTCTGGGTCTCCATCTCTCTCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTATTTTT
TGGCCCTCAGTCTATCTCTGTTTCTGCTCTCCCTGTCTGTGTATGGTCACTCTGTTCT
TCTCCCTGTCTGTTTCTCTGTCCCTATCTGTCTGTATCTCTTCTTGCTGTTTAGCTCT
CTCCCTGCGCTGTCCATCCATCTTCCCTGCTCCCTGTCTCTCTCTGTGTGGGTTCAGC
[C, G, Ast]
CCAACCTGCTCCCTCTGCCTGGCTCCATCACAGCCTACCTCCCTGCCCCATTCCCCC
AGGACGCCCATTCGATCCCTCCCTGCTGCTGGGCCAGGCCACCTCAAACGTAGTCTGCTC
CTCTCTCTTGGCTCTCCGCTTCTCTATGAGGAAGAAGGTCACCGCTGGTGGCGGG
AGCTGGTGGTACCCTGCTGGGAGTCAAGCTCCAAGGGGGCTCAGGTGAGTGGGTGGGACC
CTCTCCAACCTACCTTCCCTGAAGGTTCTGCAAGGTCCCATGAGAACTAGCTGCCCTTC

GTGGGTGGGACCCCTCTCCAACACCTTCCCTGAAGGTTCTGCAAGGTCCCATGAGAA
CTAGCTGCCCTTCTCCCCACAGCTACAGATGTTCTCTGTTTCTGCGGCCCTGCC
AGGCCCCACAAGCAGCTCTCACCACCTGCAGCAGCTTGGCTGCCCTCAGATCGGGCA
GGTGACGACGACCAAGGGGAACCTGGATGCTTCGGGCCCGCAGCTGACCTTGTGATGC
CTTCTGCTGAAGATGGCACAGGTGTGGGAAGGGTGCAGGGACCCCTCTCTGAATGGGC
[C, T, G]
TGGTGAACCTGGCAGGTCCAGCCAGGTGTCCCTGGGGACCTCAATTGGGTTCTCTCTCT
TTCTCTCTCTGCATGTCTCTGTGAGTATGAGTGTCTCTGTGATGTGTGTGCATCCCTTC
TCTGCACATCTGTCTGGCCCTTGTGAGGCGTTGTGCTCACTGCTCTCCCGCCCCGAC
TCGGCAATTTGTGCCGGGTGTCTGTCTCTCAGCATCTCTCTCTTCTCCCTCCACAC
TCGGCCCTTGTGTTCAAGGCCCATGCCAGGGTCTACACCAGCAATCCCAAGGATCACT

ATCTGTGCTGGCCCTTT CAGGGCGTTGCTCTACTGCCTCTCCCGCCCCGACCTGGGCA
TTTGTGCGGGGCTGTCTGTCTCTCAGCATTCTCTCTTTCTCCCTCCACCTCGGGCC
TTGTGTT CAGGCCCATGCCAGGGTCTACACGCAATCCCCAGGATCACTTCATCC
ATCCCTCAGCCTCCCCAGACTTTATGTAAATT CACAATTTATGTGAATTGTGCTCA
TTTATTAGGAAGCCTTGCAATATCAAGTTATGTTAATAAAGTCCACTTTATTAATTAT
[T, A, A]
AGAACAAATATTTCTTTCTTTTTTTTTCTTTTCTTTTAAAGAGACAGGATCTCTTC
TGTTGCCCAAGCTAGAGTACAGTTGCAAAATCATAGCTCACTGCAACCTTGAACCTCTGG
GCTCAAGCAATCCTCTGCCTCGGGCTCTGATAGCTGGGACAACAGGTGTGCACCACC
ACACCTGGCTAAATTTTTTTTTTTTTCTTTCTGTAGAGATAGACTCTACTATGTATCCGAG
CTGGTCTTGAATTCCTGGGCTCATGTAATCCTCCTGCTGCCTTGAACCTCCAAAGGCTGTG

TCTTTAATTAAGTGCAGCTCCCTGTTTGTGGAGAAAGAAAAATTTTTCTAACCCATT
GCCCAATTTCTTTTCTTTTATTAATATTTTTAGTTTTAACTATAGTAAATACACA
TAACGTTTACCACCTTAACCAATTTTAGTATACAGTACAGTAGTGTTCAGTACATTT
CACTGTATGCAATCAGTCTCCAGAACTCTTCATGTGCAAGCTGAAACTCTATACCA
TAAACAACCTGCTGTTCTCTCTCTCCAACCCTGGCAATCACCTTTTTTTTTTGAGA
[C, T]
GAAGTCTCACTCTGTCAACCAGGCTAGAGTGGCGTGGCTCAGCTCGGCTCACTGCAAGC
TCCGCTCCCGGGTCTAGTCCATTCTCTGCTCAGTCTCCAAGCAGCTGGGACTACAG
GTGCGCGTCAACCACGCTGCTGCTAATTTTTGTATTTTTAGTAGAGATGGAGTTTCATCGT
GTAGCCAGGCTGATCTCAAACCTCTGGCTCAAGTATCCACCGCTCGGCTGCCAAC
AGTGTCTGGGACTACAGGCGTGAGCCACTGTGCTGGCCAGGAAGTAGACTCTTGATATTA

CTGTCTTCTCTCTTTTCTCTCTTTCTTTCTTGACAGGGTCTCTTTGTCTCCAGGCTG
GGGTGCAGTGGTACAGCATAGCTCACAGCAGCCTTGAACCTCTAGGCTCAAGTGATCCT
CCCAGCTCAGCCTCCTGAGCAGCTGGGACCAAGGGCTCATACACCACTGCCTGGCTAATT
TTTAAATTTTCGTAGAGACAAGGTCTGTTATATTGCCAGGCTGGTCTCAAACTCTG
GGCTCAAATGCTTCTCTCACCTCAGCCTCCACGTGGCTGGGATTACAGGCATGAGCCAC
[G, C, T]
GCAGCGCACTCAACACTCCACAAATGTTGATGCCATTATGTTTTGTGAAGTAGTGCCCT
GGCACCCGAGACTTGTACTCCAACTCGAGGACCAAAATAGACTGGGGTGGGAAGGGGTTT
ATAGTTTTCATTATTATTTCCCTCAGGGCAGCGAGGCTCTCCCTCTGCTTGGCTCCATCC
TGCATGCCCCCAACATCTTCAAGCACAAGCAAGATTCAACCAGACCGTTTCTGGATG
CAGATGGACGGTTCAGGAAGCATGAGGCGTTCTGCCCTTCTCCTTAGGTATCTGCTGCA

FIGURE 3H

DEC 20 2002
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Docket No.: CL000685
Serial No.: 09/748,127
Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN DRUG-METABOLIZING...

12973 CTGTCTTCTCTCTTTCTCTCTTTCTTTCTTGACAGGGTCTCTCTTTGTCTCCAGGCTG
GGGTGCACTGGGTACAAGCATAGCTCACAGCAGCCTTGAACCTCTAGGCTCAAGTGATCCT
CCCACGTGAGCCTCTGAGCAGCTGGGACAACGGGCTCATACCACCATGCCGGCTAATT
TTTTAATTTTTCTGAGAGACAAGGTCTTGTATATTGCCAGGCTGGTCTCAAACCTCTG
GGCTCAAATGCTTCTCTCACCTCAGCCTCCCACGTGGCTGGGATTACAGGCATGAGCCAC
[A, G, T]
GCACGCCACTCAACACTCCACAAATGTTGATGCCATTATGTTTTGTGAAGTGTCTCCCT
GGCAGCCGAGACTTGTACTCCACACTCGAGGACCAATAGACTGGGGTGGGAAGGGGTTT
ATAGTTTCATTATTATTTCCCTCAGGGCACGGAGGTCTTCCCTCTCTTGCTCCATCC
TGCATGACCCCAACATCTTCAAGCACCCAGAAGAGTTCAACCCAGACCGTTTCTGGATG
CAGATGGACGGTTCAGGAAGCATGAGGCGTTCTGCCCTTCTCTTAGGTATCTGCTGCA

13012 CTCTCTTTGTCTCCAGGCTGGGGTGCACTGGTACAAGCATAGCTCACAGCAGCCTTGAA
CTCCTAGGCTCAAGTGATCCTCCCACGTGAGCCTCTGAGCAGCTGGGACAACGGGCTCA
TACCACCATGCCGGCTAATTTTTAATTTTTCTGAGAGACAAGGTCTTGTATATTGCC
CAGGCTGGTCTCAAACCTCTGGGCTCAAATGCTTCTCTCACCTCAGCCTCCCACGTGGCT
GGGATTACAGGCATGAGCCACTGCACGCCACTCAACACTCCACAAATGTTGATGCCATTA
[G, A, C, S, T]
GTTTTGTGAAGTGTCTCCCTGGCAGCCGAGACTTGTACTCCACACTCGAGGACCAATA
GACTGGGGTGGGAAGGGGTTATAGTTTCATTATTATTTCCCTCAGGGCACGGAGGTCT
TCCCCCTCTTGGCTCCATCTGATGACCCCAACATCTTCAAGCACCCAGAAGAGTTCA
ACCCAGACCGTTTCTGGATGCAGATGGACGGTTCAGGAAGCATGAGGCGTTCTGCCCT
TCTCCTTAGGTATCTGCTGCAGCCTGGGTATCACAAGCAGGTGCTGGCGAACTCCAGGC

13072 CTCCTAGGCTCAAGTGATCCTCCCACGTGAGCCTCTGAGCAGCTGGGACAACGGGCTCA
TACCACCATGCCGGCTAATTTTTAATTTTTCTGAGAGACAAGGTCTTGTATATTGCC
CAGGCTGGTCTCAAACCTCTGGGCTCAAATGCTTCTCTCACCTCAGCCTCCCACGTGGCT
GGGATTACAGGCATGAGCCACTGCACGCCACTCAACACTCCACAAATGTTGATGCCATTA
TGTTTTGTGAAGTGTCTCCCTGGCAGCCGAGACTTGTACTCCACACTCGAGGACCAAT
[A, T, C, S, G]
GACTGGGGTGGGAAGGGGTTATAGTTTCATTATTATTTCCCTCAGGGCACGGAGGTCT
TCCCCCTCTTGGCTCCATCTGATGACCCCAACATCTTCAAGCACCCAGAAGAGTTCA
ACCCAGACCGTTTCTGGATGCAGATGGACGGTTCAGGAAGCATGAGGCGTTCTGCCCT
TCTCCTTAGGTATCTGCTGCAGCCTGGGTATCACAAGCAGGTGCTGGCGAACTCCAGGC
ATCTGTGCCAGCTGGGGGCACCTTCTGCACCTGGGCTTACTGTTGGCTCTCCACCTG

13370 ATAGACTGGGGTGGGAAGGGGTTTATAGTTTCATTATTATTTCCCTCAGGGCACGGAGG
TCTTCCCCCTCTTGGCTCCATCTGATGACCCCAACATCTTCAAGCACCCAGAAGAGT
TCAACCCAGACCGTTTCTGGATGCAGATGGACGGTTCAGGAAGCATGAGGCGTTCTGCTG
CCTTCTCCTTAGGTATCTGCTGCAGCCTGGGTATCACAAGCAGGTGCTGGCGAACTCCA
GGCATCTGTGCCAGCTGGGGGCACCTTCTGCACCTGGGCTTACTGTTGGCTCTCCAC
[C, G]
TGCTGTTCCCCCGTGGGCTGGGTGTGAGGAATACTGACTCAGCCCTCTCTCTCTCTCT
CTCCTCACCAGGGAAGCGTGTCTGCCCTGGAGAGGGCTGGCAAAAGCGGAGCTCTTCTCT
CTTCTTCAACACCATCTTCAAGCCTTCTCCCTGGAGAGCCGTGCCCGCCGGTACACCC
TGAGCCTCAAGCCCACCGTCAAGTGGCTTTTCAACATTCCCCAGCCTTCCAGCTGCAAG
TCCGTCCCACTGACCTTCACTCCACCACGAGACAGATGAAGGAAGGCAACTTGAAGT

13682 CCGTGGGCTGGGTGTGAGGAATACTGACTCAGCCCTCTCTCTCTCTCTCTCTCCTCACCAG
GGAAGCGTGTCTGCCCTGGAGAGGGCTGGCAAAAGCGGAGCTCTTCTCTTCTTCAACA
CCATCCTACAAGCCTTCTCCCTGGAGAGCCGTGCCCGCCGGTACACCTGAGCCTCAAG
CCCACCGTCAAGTGGCTTTTCAACATTCCCCAGCCTTCCAGCTGCAAGTCCGTCCCACT
GACCTTCACTCCACCACGAGACAGATGAAGGAAGGCAACTTGAAGTGGTGGGTGCC
[C, T, A]
GGACGGTGCCTCCAGCCTCAACAGTGGGATGGACAGGGTTAATGTCTCCAGAGTGTACA
CTGAGGCAGCCACATTTACACGCTGAGTTGTTTTCCGGAGTCTGTCCACGGGCCAC
ACGCTCACTTGAATGCTGCTAAGATGCACAACCGCACCCATACACAATAAAGG
GCCACAAAGCAACTGCTGGGTAGCTTTCCACAGACATAAATATAGTCCATCTGCAATCA
CAAGCACATAGCCAGGTAACCCACCACTCCCTGGATCTGCAGCCACACGTGGGAGTC

FIGURE 3I



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Inventors: YAN, Chunhua et al.
Title: ISOLATED HUMAN DRUG-METABOLIZING...

14631

GCAGCCCTCAGTCACCCCTTTTAAAGCACCTGATTCTACCAAATGCAAACACATCTGGG
TCTGCGATTATGCACAGAGACTTTGGACATACGAGGACCCTCAGACCGGAGGAACACCTG
CCCAACCCCAACACGTGCTTATGTAACCACGTGGAAAGCGGCCCTGCTGCCCTCCACA
CACACATACACACTCACTGATCTACAGCCCTGTTGCGCGTCAGAGTCCCCACTAGACCC
AGTGGAAAGGGTTAGAGACCAAGTAGGGGCCAGTTTCCAATTCACCTGTCAGGGAGTGA
[C,T,G]
CCGGATCTGACGTTCTTGTGACTTAAGGGTCCGGCTTGGGAATTAAGTTTGTCTGG
CCTTTAGCCTACTGCGTGTGTGACCCGTGTGAGTCACTGTGAGTAAGGGTGGGACAGG
GGAGTCCACCCCTCCCCTGAGGCTGGGCGGGAGCTGAAAAACATGGCCACCGCCACCCT
GGCTGTTGACATCAGGACCAGATGTGGAGCTGGGAGGAGGGCAGGGCTGGTGACGCCCT
GGGCCTCATTTCCAAAAAGGGCCAAGGTGTCCGGCGTGGGAAGTGGCAAGGAGGGGT

Chromosomal Map Position

ePCR to dbSTS

Site (bases)	Marker	Chr.	Organism
15155..15288	stSG46708	19	Homo sapiens

FIGURE 3J